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```
    CGTCCGGCGGAAGGCGACATGGGCTCCGCTCCCTGGGCCCCGGTCCTGCTGCTGGCGCTC
  1 ---------+---------+---------+---------+---------+---------+ 60
                      M  G  S  A  P  W  A  P  V  L  L  L  A  L   -

    GGGCTGCGCGGCCTCCAGGCGGGGGGCCCGCAGGGCCCCGGACCCCGGCTTCCAGGAGCGC
 61 ---------+---------+---------+---------+---------+---------+ 120
     G  L  R  G  L  Q  A  G  A  R  R  A  P  D  P  G  F  Q  E  R   -

    TTCTTCCAGCAGCGTCTGGACCACTTCAACTTCGAGCGCTTCGGCAACAAGACCTTCCCT
121 ---------+---------+---------+---------+---------+---------+ 180
     F  F  Q  Q  R  L  D  H  F  N  F  E  R  F  G  N  K  T  F  P   -

    CAGCGCTTCCTGGTGTCGGACAGGTTCTGGGTCCGGGGCGAGGGGCCCATCTTCTTCTAC
181 ---------+---------+---------+---------+---------+---------+ 240
     Q  R  F  L  V  S  D  R  F  W  V  R  G  E  G  P  I  F  F  Y   -

    ACTGGGAACGAGGGCGACGTGTGGGCCTTCGCCAACAACTCGGGCTTCGTCGCGGAGCTG
241 ---------+---------+---------+---------+---------+---------+ 300
     T  G  N  E  G  D  V  W  A  F  A  N  N  S  G  F  V  A  E  L   -

    GCGGCCGAGCGGGGGGGCTCTACTGGTCTTCGCGGAGCACCGCTACTACGGGAAGTCGCTG
301 ---------+---------+---------+---------+---------+---------+ 360
     A  A  E  R  G  A  L  L  V  F  A  E  H  R  Y  Y  G  K  S  L   -

    CCGTTCGGTGCGCAGTCCACGCAGCGCGGGCACACGGAGCTGCTGACGGTGGAGCAGGCC
361 ---------+---------+---------+---------+---------+---------+ 420
     P  F  G  A  Q  S  T  Q  R  G  H  T  E  L  L  T  V  E  Q  A   -

    CTGGCCGACTTCGCAGAGCTGCTCCGCGCGCTACGACGCGACCTCGGGGCCCAGGATGCC
421 ---------+---------+---------+---------+---------+---------+ 480
     L  A  D  F  A  E  L  L  R  A  L  R  R  D  L  G  A  Q  D  A   -

    CCCGCCATCGCCTTCGGTGGAAGTTATGGGGGGATGCTCAGTGCCTACCTGAGGATGAAG
481 ---------+---------+---------+---------+---------+---------+ 540
     P  A  I  A  F  G  G  S  Y  G  G  M  L  S  A  Y  L  R  M  K   -

    TATCCCCACCTGGTGGCGGGGGCGCTGGCGGCCAGCGCGCCCGTTCTAGCTGTGGCAGGC
541 ---------+---------+---------+---------+---------+---------+ 600
     Y  P  H  L  V  A  G  A  L  A  A  S  A  P  V  L  A  V  A  G   -

    CTCGGCGACTCCAACCAGTTCTTCCGGGACGTCACGGCGGACTTTGAGGGCCAGAGTCCC
601 ---------+---------+---------+---------+---------+---------+ 660
     L  G  D  S  N  Q  F  F  R  D  V  T  A  D  F  E  G  Q  S  P   -

    AAATGCACCCAGGGTGTGCGGGAAGCGTTCCGACAGATCAAGGACTTGTTCCTACAGGGA
661 ---------+---------+---------+---------+---------+---------+ 720
     K  C  T  Q  G  V  R  E  A  F  R  Q  I  K  D  L  F  L  Q  G   -
```

FIG. 1A.

Title: 22012, A Novel Human Carboxypeptidase
Inventor(s): Kapeller-Libermann et al.
Application No: Not Assigned
Atty Dkt No: 35800/243653(5800-38A)

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```
     GCCTACGACACGGTCCGCTGGGAGTTCGGCACCTGCCAGCCGCTGTCAGACGAGAAGGAC
721  ---------+---------+---------+---------+---------+---------+  780
      A  Y  D  T  V  R  W  E  F  G  T  C  Q  P  L  S  D  E  K  D   -

     CTGACCCAGCTCTTCATGTTCGCCCGGAATGCCTTCACCGTGCTGGCCATGATGGACTAC
781  ---------+---------+---------+---------+---------+---------+  840
      L  T  Q  L  F  M  F  A  R  N  A  F  T  V  L  A  M  M  D  Y   -

     CCCTACCCCACTGACTTCCTGGGTCCCCTCCCTGCCAACCCCGTCAAGGTGGGCTGTGAT
841  ---------+---------+---------+---------+---------+---------+  900
      P  Y  P  T  D  F  L  G  P  L  P  A  N  P  V  K  V  G  C  D   -

     CGGCTGCTGAGTGAGGCCCAGAGGATCACGGGGCTGCGAGCACTGGCAGGGCTGGTCTAC
901  ---------+---------+---------+---------+---------+---------+  960
      R  L  L  S  E  A  Q  R  I  T  G  L  R  A  L  A  G  L  V  Y   -

     AACGCCTCGGGCTCCGAGCACTGCTACGACATCTACCGGCTCTACCACAGCTGTGCTGAC
961  ---------+---------+---------+---------+---------+---------+  1020
      N  A  S  G  S  E  H  C  Y  D  I  Y  R  L  Y  H  S  C  A  D   -

     CCCACTGGCTGCGGCACCGGCCCCGACGCCAGGGCCTGGGACTACCAGGCCTGCACCGAG
1021 ---------+---------+---------+---------+---------+---------+  1080
      P  T  G  C  G  T  G  P  D  A  R  A  W  D  Y  Q  A  C  T  E   -

     ATCAACCTGACCTTCGCCAGCAACAATGTGACCGATATGTTCCCCGACCTGCCCTTCACT
1081 ---------+---------+---------+---------+---------+---------+  1140
      I  N  L  T  F  A  S  N  N  V  T  D  M  F  P  D  L  P  F  T   -

     GACGAGCTCCGCCAGCGGTACTGCCTGGACACCTGGGGCGTGTGGCCCCGGCCCGACTGG
1141 ---------+---------+---------+---------+---------+---------+  1200
      D  E  L  R  Q  R  Y  C  L  D  T  W  G  V  W  P  R  P  D  W   -

     CTGCTGACCAGCTTCTGGGGGGGTGATCTCAGAGCCGCCAGCAACATCATCTTCTCCAAC
1201 ---------+---------+---------+---------+---------+---------+  1260
      L  L  T  S  F  W  G  G  D  L  R  A  A  S  N  I  I  F  S  N   -

     GGGAACCTGGACCCCTGGGCAGGGGGCGGGATTCGGAGGAACCTGAGTGCCTCAGTCATC
1261 ---------+---------+---------+---------+---------+---------+  1320
      G  N  L  D  P  W  A  G  G  G  I  R  R  N  L  S  A  S  V  I   -

     GCCGTCACCATCCAGGGGGGGAGCGCACCACCTCGACCTCAGAGCCTCCCACCCAGAAGAT
1321 ---------+---------+---------+---------+---------+---------+  1380
      A  V  T  I  Q  G  G  A  H  H  L  D  L  R  A  S  H  P  E  D   -

     CCTGCTTCCGTGGTTGAGGCGCGGAAGCTGGAGGCCACCATCATCGGCGAGTGGGTAAAG
1381 ---------+---------+---------+---------+---------+---------+  1440
      P  A  S  V  V  E  A  R  K  L  E  A  T  I  I  G  E  W  V  K   -

     GCAGCCAGGCGTGAGCAGCAGCCAGCTCTGCGTGGGGGGCCCAGACTCAGCCTCTGAGCA
1441 ---------+---------+---------+---------+---------+---------+  1500
      A  A  R  R  E  Q  Q  P  A  L  R  G  G  P  R  L  S  L       -

     CAGGACTGGAGGGGTCTCAAGGCTCCTCATGGAGTGGGGGCTTCACTCAAGCAGCTGGCG
1501 ---------+---------+---------+---------+---------+---------+  1560
```

FIG. 1B.

```
     GCAGAGGGAAGGGGCTGAATAAACGCCTGGAGGCCTGGCAAAAAAAAAAAAAAAAAAAAAA
1561 ---------+---------+---------+---------+---------+---------+ 1620

     AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
1621 ---------+---------+---------+--- 1653
```

FIG. 1C.

```
------------------------------------------------------------------
 Query:  22012
Scores for sequence family classification (score includes all domains):
Model       Description                              Score  E-value  N
------      -----------                              -----  -------  -
abhydrolase  alpha/beta hydrolase fold                31.8  1.6e-05  1
Peptidase_S9 Prolyl oligopeptidase family             8.4   0.25    1

Parsed for domains:
Model        Domain  seq-f  seq-t   hmm-f  hmm-t     score  E-value
------       ------  -----  -----   ----- ------     -----  -------
Peptidase_S9  1/1     158    167 ..    72    81 .)     8.4   0.25
abhydrolase   1/1     100    360 ..     1   233 ()    31.8  1.6e-05

Alignments of top-scoring domains:
Peptidase_S9: domain 1 of 1, from 158 to 167:  score 8.4, E = 0.25
                    *->ifGgSnGGiL<-*
                       +fGgS+GG+L
       22012    158   AFGGSYGGML     167

abhydrolase:  domain 1 of 1, from 100 to 360: score 31.8, E = 1.6e-05
                    *->frvialDlrGfGeSsrp...........sdladyrfddlaedleal
                       + ++ + +r++G+S  p + +++++++++++ + +    +d+ae l al
       22012    100   ALLVFAEHRYYGKSL-PfgaqstqrghteLLTVEQALADFAELLRAL 145

                    ldalgldkp.vilvGhSmGGalaaayaakyPeervkalvlvstp....ap
                    ++ lg + ++i++G+S+GG+l+a++++kyP+ +v+++ + s+p    a
       22012    146   RRDLGAQDApAIAFGGSYGGMLSAYLRMKYPH-LVAGALAASAPvlavAG 194

                    aglssrlfprlgnleglllanffnrlsrsveallgralkqffllgrpfvs
                    g s+ +f++ ++ ++ ++ ++++       +ea++++ +  +fl g +
       22012    195   LGDSNQFFRDVTADFEGQSPKCTQ---GVREAFRQIKD--LFLQGAY--- 236

                    dflkqaedwlsslarp.getdggdglly...avalgkllqwdrs.alkd
                    d ++++++++ l++++ t+ ++   ++ +  + + + +d+ ++l+
       22012    237   DTVRWEFGTCQPLSDEkDLTQLFMFARNAftvLAMMDYPYPTDFLgPLPA 286

                    ..ikvPtlviwgddDplvplkaseklsalfpna.evvviddagHla....
                    +++kv  + +  +++ l a   l + ++++ +++i +H    +++
       22012    287   npVKVGCDRLLSEAQRITGLRALAGLVYNASGSeHCYDIYRLYHSCadpt 336

                    ........llekpeevaeli.kfl<-*
                    + +++++  ++++++++e+   f+
       22012    337   gcgtgpdaRAWDYQACTEINlTFA     360
 //
```
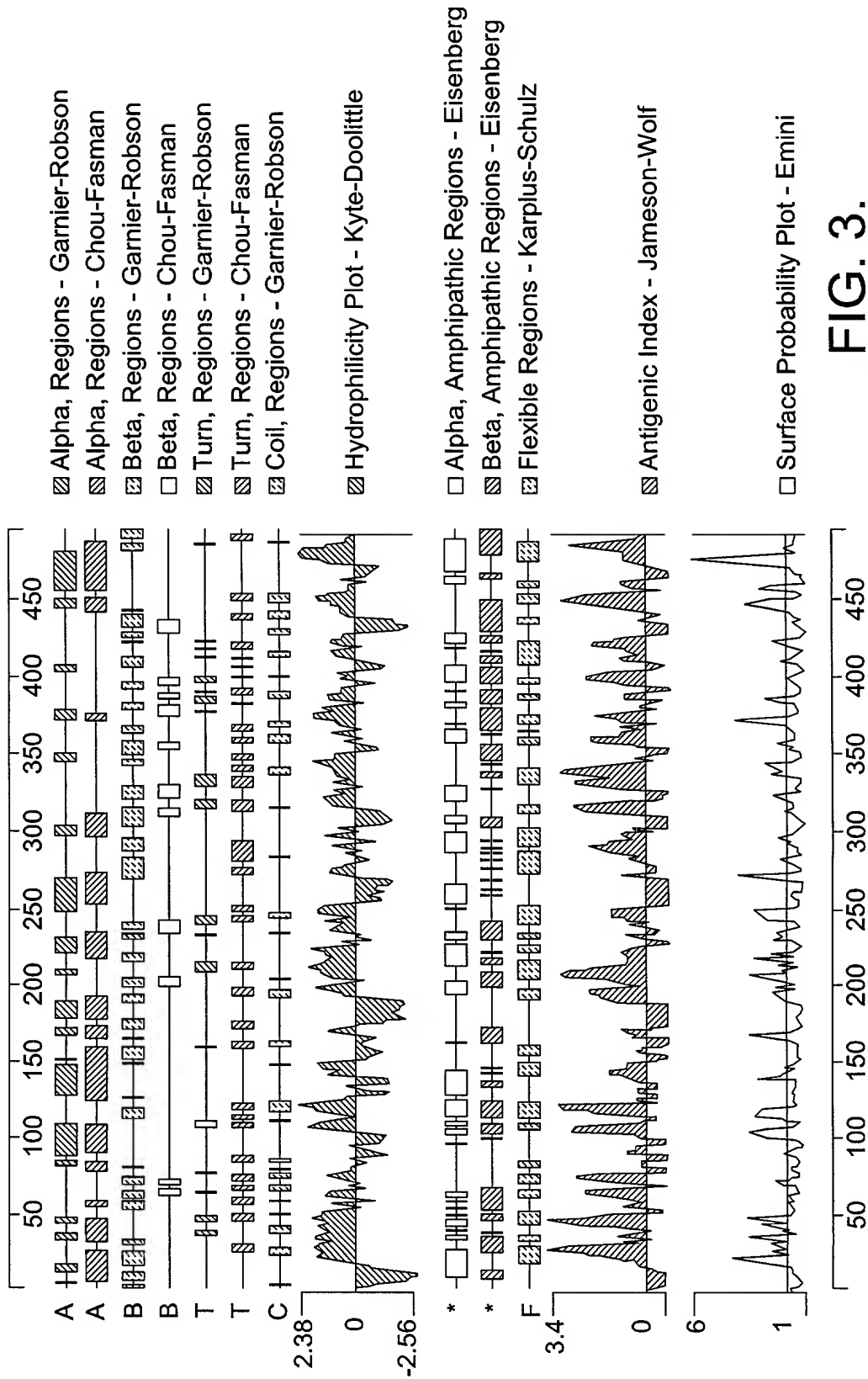
FIG. 2.

▨	Alpha, Regions - Garnier-Robson
▨	Alpha, Regions - Chou-Fasman
▨	Beta, Regions - Garnier-Robson
☐	Beta, Regions - Chou-Fasman
▨	Turn, Regions - Garnier-Robson
▨	Turn, Regions - Chou-Fasman
▨	Coil, Regions - Garnier-Robson
▨	Hydrophilicity Plot - Kyte-Doolittle
☐	Alpha, Amphipathic Regions - Eisenberg
▨	Beta, Amphipathic Regions - Eisenberg
▨	Flexible Regions - Karplus-Schulz
▨	Antigenic Index - Jameson-Wolf
☐	Surface Probability Plot - Emini

FIG. 3.

Title: 22012, A Novel Human Carboxypeptidase
Inventor(s): Kapeller-Libermann et al.
Application No: Not Assigned
Atty Dkt No: 35800/243653(5800-38A)
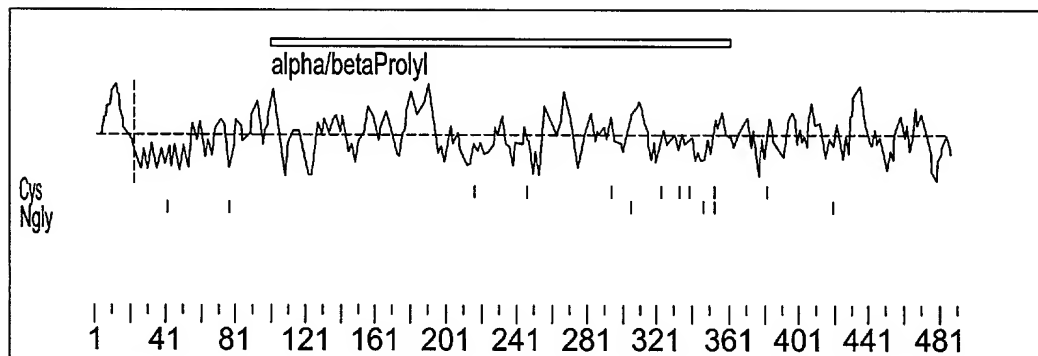
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Analysis of 22012 (492 aa)

>22012
MGSAPWAPVLLLALGLRGLQAGARRAPDPGFQERFFQQRLDHFNFERFGNKTFPQRFLVS
DRFWVRGEGPIFFYTGNEGDVWAFANNSGFVAELAAERGALLVFAEHRYYGKSLPFGAQS
TQRGHTELLTVEQALADFAELLRALRRDLGAQDAPAIAFGGSYGGMLSAYLRMKYPHLVA
GALAASAPVLAVAGLGDSNQFFRDVTADFEGQSPKCTQGVREAFRQIKDLFLQGAYDTVR
WEFGTCQPLSDEKDLTQLFMFARNAFTVLAMMDYPYPTDFLGPLPANPVKVGCDRLLSEA
QRITGLRALAGLVYNASGSEHCYDIYRLYHSCADPTGCGTGPDARAWDYQACTEINLTFA
SNNVTDMFPDLPFTDELRQRYCLDTWGVWPRPDWLLTSFWGGDLRAASNIIFSNGNLDPW
AGGGIRRNLSASVIAVTIQGGAHHLDLRASHPEDPASVVEARKLEATIIGEWVKAARREQ
QPALRGGPRLSL

FIG. 4.

Prosite Pattern Matches for 22012

Prosite version: Release 12.2 of February   1995

>PS00001/PDOC00001/ASN_GLYCOSYLATION N-glycosylation site.

Query:	50	NKTF	53
Query:	86	NNSG	89
Query:	315	NASG	318
Query:	356	NLTF	359
Query:	363	NVTD	366
Query:	428	NLSA	431

>PS00005/PDOC00005/PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query:	60	SDR	62
Query:	121	TQR	123
Query:	213	SPK	215
Query:	238	TVR	240

>PS00006/PDOC00006/CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query:	75	TGNE	78
Query:	317	SGSE	320
Query:	331	SCAD	334
Query:	340	TGPD	343
Query:	450	SHPE	453
Query:	457	SVVE	460

>PS00008/PDOC00008/MYRISTYL N_myristoylation site.

Query:	18	GLQAGA	23
Query:	117	GAQSTQ	122
Query:	160	GGSYGG	165
Query:	181	GALAAS	186
Query:	194	GLGDSN	199
Query:	219	GVREAF	224
Query:	234	GAYDTV	239
Query:	311	GLVYNA	316
Query:	318	GSEHCY	323
Query:	424	GIRRNL	429

>PS00029/PDOC00029/LEUCINE_ZIPPER Leucine zipper pattern.

Query:	128	LLTVEQALADFAELLRALRRDL	149

FIG. 5.

22012 TAQMAN RESULTS

RELATIVE EXPRESSION

30.00
25.00
20.00
15.00
10.00
5.00
0.00

	Relative Expression
Breast CA	11.96
Breast CA	12.30
Breast CA	24.42
Breast N	4.61
Breast N	2.59
Lung SCC	5.82
Lung Adeno	2.71
Lung N	2.18
Lung N	2.45
Colon Met	3.63
Colon Met	3.57
Liver N	1.76
Liver N	3.64
Colon CA	2.18
Colon CA	6.17
Colon N	1.00
Colon N	3.01

FIG. 6.

Title: 22012, A Novel Human Carboxypeptidase
Inventor(s): Kapeller-Libermann et al.
Application No: Not Assigned
Atty Dkt No: 35800/243653(5800-38A)

Gene 22012 Expression in Normal Human Tissues

Tissue Type	Relative Expression
Lymph node	2.6
Tonsil	3.9
Esophagus*	1.7
Spleen	2.3
Cervix	1.7
Small Intestine	1.9
Osteoblasts (dif.)	3.2
Fetal Heart*	1.7
Fetal Heart	7.8
Fetal Liver	13.1
Fetal Liver	3.2
Fetal Kidney	6.1
Fetal Kidney	3.3
Placenta	2.6
Thyroid	8.6
Thyroid	8.0
Testis	12.1
Testis	32.4
Vein	1.0
Vein	1.6
Lung	1.6
Lung	2.1
Kidney	4.5
Ovary	1.4
Ovary	3.0
Heart	3.9
Heart	5.6
Colon	1.5
Colon	2.2
Brain	15.2
Skeletal Muscle	6.9
Skeletal Muscle	3.2
Breast	8.3
Breast *	3.7
Liver	1.4
Prostate	11.7
Prostate	4.5

Relative Expression (Vein as Reference, Log Scale)

100 10 1

FIG. 7.

Title: 22012, A Novel Human Carboxypeptidase
Inventor(s): Kapeller-Libermann et al.
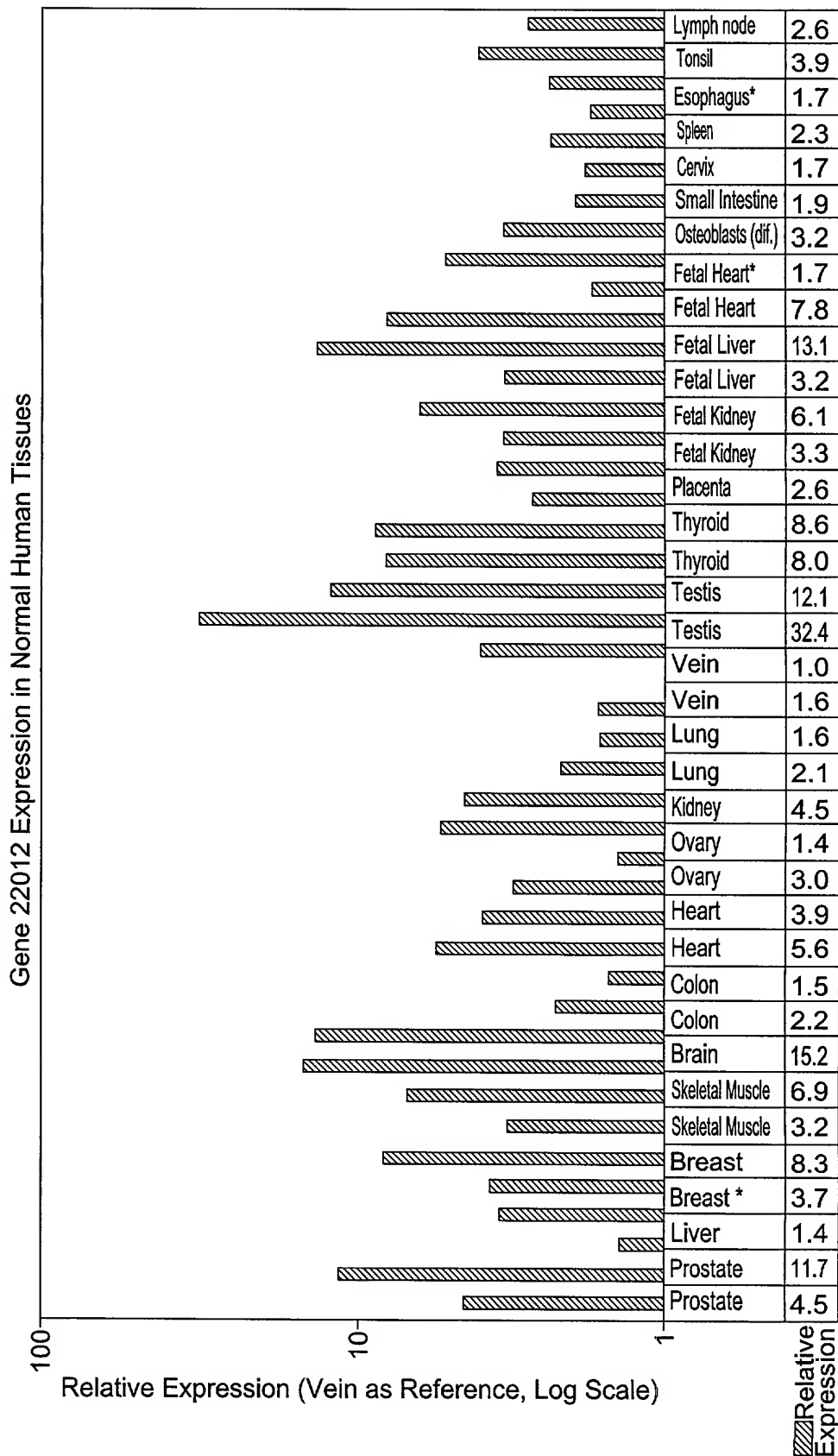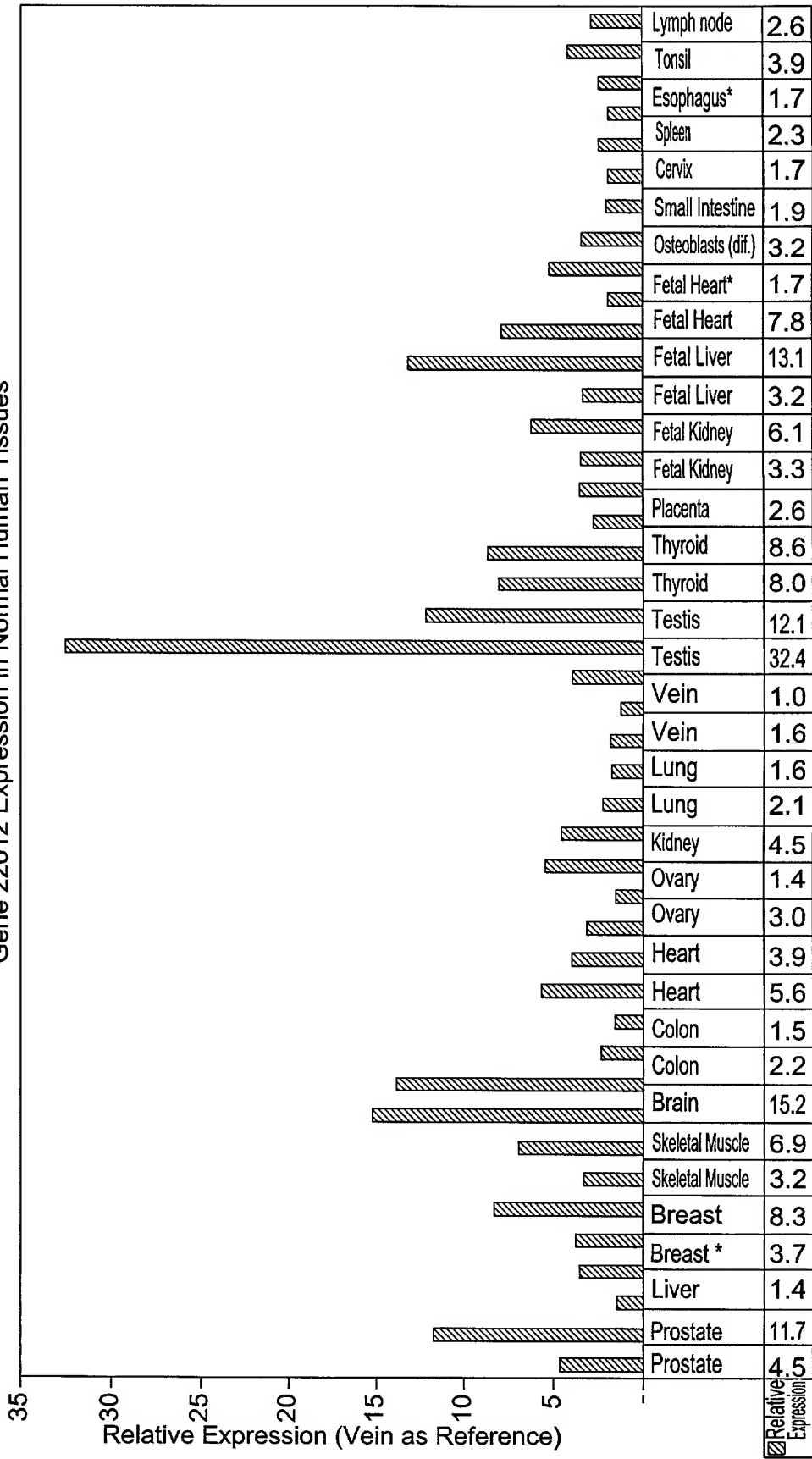Application No: Not Assigned
Atty Dkt No: 35800/243653(5800-38A)

Gene 22012 Expression in Normal Human Tissues

Tissue Type	Relative Expression
Lymph node	2.6
Tonsil	3.9
Esophagus*	1.7
Spleen	2.3
Cervix	1.7
Small Intestine	1.9
Osteoblasts (dif.)	3.2
Fetal Heart*	1.7
Fetal Heart	7.8
Fetal Liver	13.1
Fetal Liver	3.2
Fetal Kidney	6.1
Fetal Kidney	3.3
Placenta	2.6
Thyroid	8.6
Thyroid	8.0
Testis	12.1
Testis	32.4
Vein	1.0
Vein	1.6
Lung	1.6
Lung	2.1
Kidney	4.5
Ovary	1.4
Ovary	3.0
Heart	3.9
Heart	5.6
Colon	1.5
Colon	2.2
Brain	15.2
Skeletal Muscle	6.9
Skeletal Muscle	3.2
Breast	8.3
Breast *	3.7
Liver	1.4
Prostate	11.7
Prostate	4.5

Relative Expression (Vein as Reference)

35 30 25 20 15 10 5

FIG. 8.